REMARKS/ARGUMENTS

Claims 28-35, 38-40 and 44-47 are pending in this application. Applicants note that Claims 38-40, 45 and 47 contain allowable subject matter.

Applicants note and appreciate the withdrawal of the earlier objections and rejections under 35 U.S.C. §112, first and second paragraphs, and under 35 U.S.C. §102. over Ni *et al.*

The remaining rejections of Claims 28-35, 44, and 46 under 35 U.S.C. §102 are addressed below.

Claim Rejections Under 35 U.S.C. §102

The rejection of Claims 28-35, 44 and 46 under 35 U.S.C. §102(a) as being anticipated by Yousef *et al.* was maintained. The Examiner alleges, "The sequence of a nucleic acid taught in the art is inherent to the nucleic acid itself" and "thus does not need to be disclosed by the reference in order to anticipate the claimed invention." Therefore, the Examiner concludes that "Yousef et al. do teach in the prior art an isolated nucleic acid which encodes a polypeptide having 100% identity to SEQ ID NO:194."

Applicants respectfully disagree and traverse the rejection.

First, Claims 28-35, 44 and 46 are not anticipated by Yoursef *et al.* for the reasons set forth in the Applicants' response filed on December 22, 2004.

Secondly, the Examiner, himself, has admitted that "the precise polypeptide sequence and isolated complete protein is **not** taught by the reference[.]" (See page 2 of the instant Office Action, emphasis added). The Examiner further adds, "Yousef et al. do not specifically disclose the full [nucleic acid] sequence itself in the reference[.]" (See page 3 of the instant Office Action).

Third, the Examiner is incorrectly applying the doctrine of inherent anticipation.

The Legal Standard

"A claim is anticipated only if *each* and *every* element as set forth in the claim is found, either expressly or inherently described in a single prior art reference.' *Verdegaal Bros. v. Union Oil Co. of California*, 814 F.2d 628, 631, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987).

"A gene is a chemical compound, albeit a complex one, and it is well established in our law that conception of a chemical compound requires that the inventor be able to define it so as to distinguish it from other materials, and to describe how to obtain it." *Amgen Inc. v. Chugai Pharmaceutical Co.*, 927 F.2d 1200, 1214, 18 USPQ2d 1016, 1021 (Fed. Cir. 1991), *cert. denied*, 502 U.S. 856 (1991) (emphasis added).

The Federal Circuit has further held that conception of a full-length gene does not occur until the inventor can describe the gene "by structure, formula, chemical name, or physical properties." *Fiers v. Revel*, 984 F.2d 1164, 1171, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993); *Amgen Inc. v. Chugai Pharmaceutical Co.*, 927 F.2d 1200, 1214, 18 USPQ2d 1016, 1021 (Fed. Cir. 1991), *cert. denied*, 502 U.S. 856 (1991). In other words, the conception of the DNA does not occur upon conception of a method for obtaining it. In addition, the Federal Circuit has held that "cDNA is not defined or described by the mere name 'cDNA,' even if accompanied by the name of the protein that it encodes, **but requires a kind of specificity usually achieved by means of the recitation of the sequence of nucleotides that make up the cDNA.**" *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997) (emphasis added). Accordingly, it is well established that because DNA is a molecule, an adequate description of a DNA requires a precise definition of the sequence itself and not merely a recitation of its function or a reference to a method for isolating it. *See Amgen v. HMR*, 314 F.3d 1313, 1332 (Fed. Cir. 2003).

"'Inherent' properties ... are the rare exception to the rule that a party must show possession of 'every feature' recited in the count and that 'every limitation' of the count must have been known to the inventor at the time of the alleged conception." *Hitzeman v. Rutter,* 58 USPQ2d 1161, 1167 (Fed. Cir. 2001). "Moreover, consistent with the law of inherent anticipation, an inherent property must necessarily be present in the invention described by the

count, and it must be so recognized by person of ordinary skill in the art." *Id.* (emphasis added). Accordingly, recent case law in the area of inherent anticipation has held that only if a person of ordinary skill in the art, presented with all facts, would understand that the missing structure, composition or function is always necessarily present in the cited prior art, a holding of anticipation by inherency is proper. *Atlas Powder Co. v. Ireco Inc.*, 190 F.3d 1342; 51 USPQ2d 1943 (Fed. Cir. 1999); *Schering Corporation v. Geneva Pharmaceuticals, Inc.*, 67USPQ2d 1664 (Fed. Cir 2003) (emphasis added).

Proper Application of the Legal Standard

First, Applicants respectfully submit that the coding sequence for SEQ ID NO:194 comprises 744 basepairs, while the longest of the DNA fragments disclosed in Yousef *et al.* is only 260 basepairs (see Yousef *et al.*, Table VI). Further, Yousef *et al.* do not disclose the complete amino acid sequence of SEQ ID NO:194 or of variants having at least 80% sequence identity to SEQ ID NO:194, but only short portions of the protein sequence. In fact, Yousef *et al.* only disclose sequences of three "predicted" exons each having very little identity to the entire 248 amino acid SEQ ID NO:194 sequence. Indeed, Yousef *et al.* disclose only fragments of the SEQ ID NO:194 amino acid sequence, and *provide methods* by which these fragments could later be used to determine the sequence of nucleic acids encoding the full length protein.

As mentioned above, the Court in *Fiers* specifically held that a prior conception cannot be established without the complete nucleotide sequence of a DNA. The Court stated that the existence of a workable method for preparing a DNA or a plan for obtaining the DNA did not suffice. *Fiers*, 984 F.2d 1164.

Applicants further submit that an adequate written description of a DNA requires more than a reference to a potential method for isolating it. Instead, what is required is an actual description of the DNA itself, i.e. nucleic acid sequence. *Id.* at 1170-71.

Indeed, the Federal Circuit held that knowledge of a protein sequence, along with methods for using this sequence to isolated an encoding DNA sequence, does not render the encoding DNA sequence obvious. As discussed in the M.P.E.P. §2144.09, "A prior art

disclosure of the amino acid sequence of a protein does not necessarily render particular DNA molecules encoding the protein obvious because the redundancy of the genetic code permits one to hypothesize an enormous number of DNA sequences coding for the protein." *In re Bell*, 991 F.2d 781, 785, 26 USPQ2d 1529, 1532 (Fed. Cir. 1993). In *In re Deuel,* 34 USPQ2d 1210 (Fed. Cir. 1995), the Federal Circuit held that an N-terminal protein sequence, along with known methods for isolating DNA, did not render the cDNA encoding the protein obvious. The Court stated, "until the claimed molecules were actually isolated and purified, it would have been highly unlikely for one of ordinary skill in the art to contemplate what was ultimately obtained. What cannot be contemplated or conceived cannot be obvious." *Id.* at 1215.

As the Examiner has admitted in the previous Office Action (dated July 1, 2004), "[T]he precise polypeptide sequence and isolated complete protein is not taught by the reference."

Therefore, Applicants respectfully submit that Yousef *et al.* do not expressly disclose every element set forth in the claims of the instant application, *i.e.*, Yousef *et al.* do not expressly disclose the claimed nucleic acid sequence or its encoded polypeptide sequence. Accordingly, Yousef *et al.* do not provide sufficient disclosure of the cDNA sequence to anticipate the nucleic acids sequence encoding SEQ ID NO:194, since Yousef *et al.* have not disclosed the actual nucleic acid sequence of SEQ ID NO:193 which encodes the polypeptide of SEQ ID NO:194.

Next, Applicants respectfully submit that Yousef *et al.* do not *inherently* disclose the claimed nucleic acid sequence or its encoded polypeptide sequence. As stated above, an inherent property must necessarily be present in the invention described by the prior art and it must be so recognized by person of ordinary skill in the art.

As the Examiner notes the precise polypeptide sequence and isolated complete protein is not taught by the Yousef reference. The authors state that they "have used a set of arbitrary rules to consider presence of a new gene in the genomic area of interest" following the strategy described on pages 2845-2846. By using the described strategy, they have identified nine new genes, including five genes having significant homologies with known human or animal kallikrein proteins and/or known serine proteases. One of the new genes they identified was KLK-L5, which allegedly has the 100% sequence identity to SEQ ID NO:194. The authors note

that "the preliminary exon structure and partial protein sequence" for KLK-L5 is presented in Table VI. Table VI disclosed the three predicted exons of the putative gene KLK-L5. The authors conclude on page 2851 that they "are now screening and sequencing EST clones ... of these new genes" and that their goal is "to fully characterize their mRNA sequence."

Accordingly, Applicants respectfully submit that without the explicit description of the full-length nucleic acid sequence of SEQ ID NO:193 and its encoded polypeptide sequence SEQ ID NO:194, with or without the signal peptide sequence, the Yousef reference does not provide sufficient information about the nucleic acid or polypeptide sequences to allow one skilled in the art to recognize that the undisclosed portions of SEQ ID NO:193 and SEQ ID NO:194 must necessarily be present. As the authors admit, "It is important to mention that the prediction of new genes by computer programs is still not a straightforward process. Many shortcomings are known to exist in such programs." (See page 2850, left column). For example, the authors add, "Most of these programs are unable to detect non-coding exons and non-coding portions of exons." One of ordinary skill in the art would not be able to tell which particular regions of genomic sequence were or were not part of cording regions of exons until the complete mRNA sequence had been fully characterized. Therefore, the undisclosed portions of SEQ ID NO:193 and SEQ ID NO:194 would not be obvious to one skilled in the art as necessary being present in the full-length sequences until the sequences had been fully identified. Accordingly, Applicants respectfully submit that Yousef *et al.* do not inherently describe the claimed nucleic acid sequence or its encoded polypeptide sequence.

In view of the arguments above, Applicants respectfully request the withdrawal of the rejection of Claims 28-35, 44, and 46 under 35 U.S.C. § 102(a) as being anticipated by Yousef *et al.*

CONCLUSION

All claims pending in the present application are believed to be in *prima facie* condition for allowance, and an early action to that effect is respectfully solicited.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. **08-1641**, referencing Attorney's Docket No. **39780-2830 P1C51**). Please direct any calls in connection with this application to the undersigned at the number provided below.

Respectfully submitted,

Date: May 24, 2005

By: _____
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